

Automatic determination of optimal cluster number

 Jakob Nikolas Kather

Updated date: Feb 20, 2020

 An abbreviated version of this protocol was published in eLIFE in Sep 2018

Topography of cancer-associated immune cells in human solid tumors

DOI: 10.7554/eLife.36967

Detailed protocol

Thank you very much for your interest in our work! The Matlab script that was used to determine the optimal number of clusters can be found here: https://github.com/elifesciences-publications/immuneTopography/blob/master/step_03b_findOptimClust.m The core function in this script is the Matlab function "evalclusters" which is extensively documented here: <https://de.mathworks.com/help/stats/evalclusters.html>. These links should allow you to reproduce the procedure for your project. Hope that helps!

How to cite: (Readers should cite both the Bio-protocol preprint and the original research article where this protocol was used)

1. Kather, J. (2020). Automatic determination of optimal cluster number. Bio-protocol Preprint. [bio-protocol.org/prep219](https://doi.org/10.21956/bio-protocol.preprint.219).
2. Kather, J. N., Suarez-Carmona, M., Charoentong, P., Weis, C., Hirsch, D., Bankhead, P., Horning, M., Ferber, D., Kel, I., Herpel, E., Schott, S., Zörnig, I., Utikal, J., Marx, A., Gaiser, T., Brenner, H., Chang-Claude, J., Hoffmeister, M., Jäger, D. and Halama, N. (2018). Topography of cancer-associated immune cells in human solid tumors. eLIFE. DOI: [10.7554/eLife.36967](https://doi.org/10.7554/eLife.36967)

Copyright: Content may be subjected to copyright.